

Summary of cosmid clones isolated from *M. echinospora* genomic library.

clone ^a	type I PKS genes ^b	type II PKS genes ^b	deoxy sugar genes ^b	resistance (μ g mL ⁻¹) ^c
3a	N.D. ^d	N.D. ^d	N.D. ^d	0.5
4a	N.D. ^d	N.D. ^d	N.D. ^d	0.5
4b	+	+	+	0.5
10a	+	+	+	0.5
13a	+	+	+	0.5
16a	N.D. ^d	N.D. ^d	N.D. ^d	0.1
56	+	+	+	< 0.01
58	-	-	+	0.05
60	+	+	+	0.04
66	-	-	-	< 0.01
puc18/pBluescript ^f	-	-	-	

Fig. 1

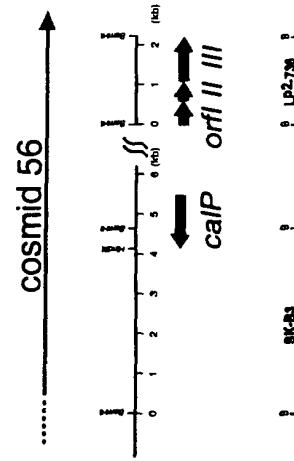
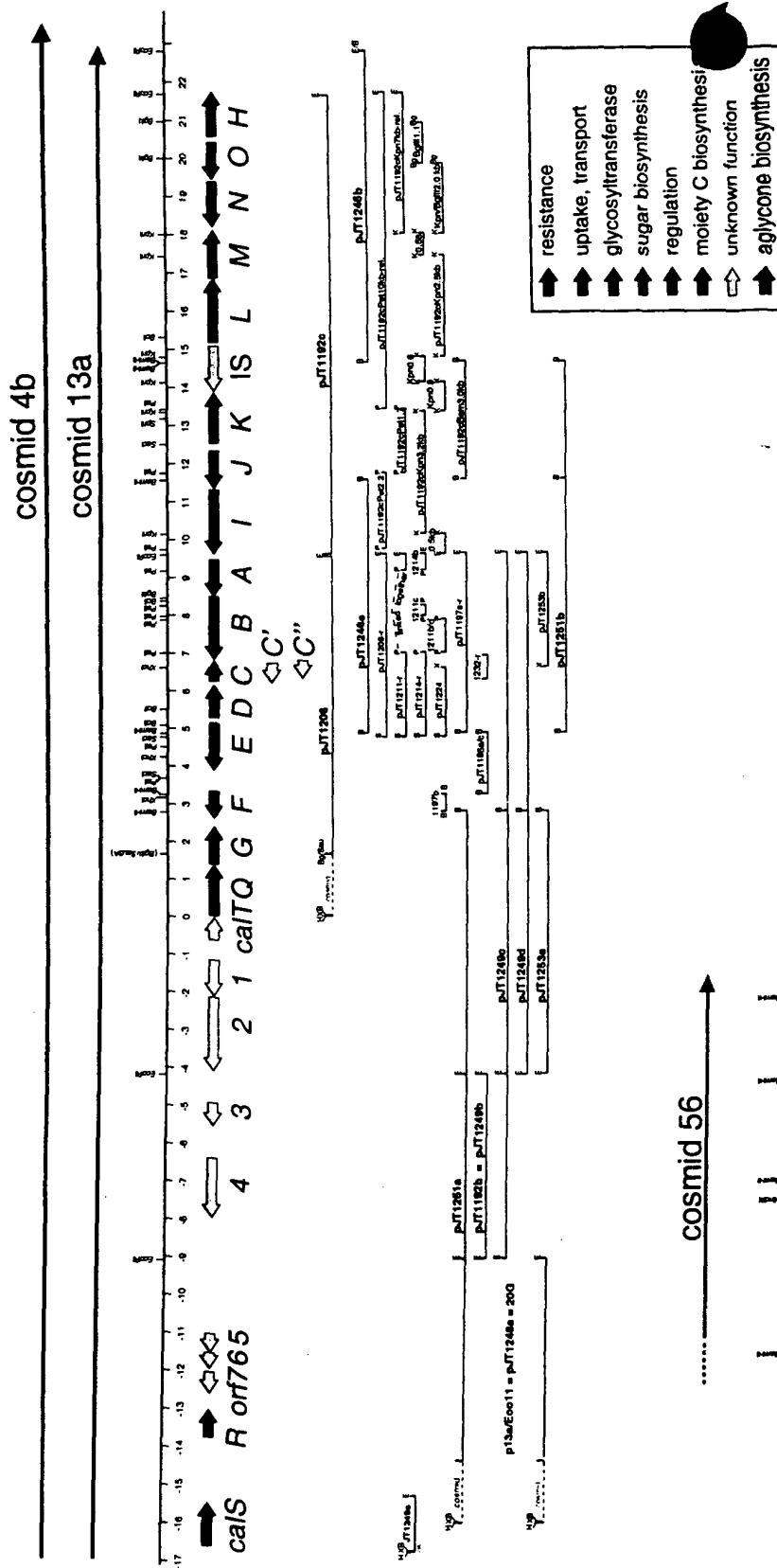
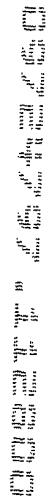


Fig. 2

putative polypeptide	number of amino acids	proposed function or sequence similarity detected ^a	probability ^b	start/stop codons	best match
CalA	328	membrane transporter (ATP-binding)	5.4×10^{-124}	ATG/TGA	DrrA ⁹⁷
CalB	561	membrane transporter	5.5×10^{-70}	ATG/TGA	DrrB ⁹⁷
CalC	181	calicheamicin resistance protein	confirmed ^c	ATG/TGA	
CalD	263	O-methyltransferase	1.1×10^{-99}	ATG/TGA	AveB ^{VII} ⁹⁸
CalE	420	Glycosyltransferase	4.7×10^{-30}	GTG/TAG	EryCII ⁹⁹
CalF	245	N,N-dimethyltransferase	1.5×10^{-78}	ATG/TGA	DesVI ¹⁰⁰
CalG	990	TDP-D-glucose 4,6-dehydratase	confirmed ^c	GTG/TAG	
CalH	338	Perosamine synthetase	confirmed ^c	GTG/TGA	
CalI	568	Dipeptide transporter	1.7×10^{-24}	GTG/TGA	DciAE
CalJ	332	O-methyltransferase	1.0×10^{-37}	ATG/TGA	DmpM
CalK	440	L-cysteine/cystine C-S-lyase	1.6×10^{-28}	GTG/TGA	C-DES
CalL	562	Oligopeptide transporter protein	9.5×10^{-14}	ATG/TGA	OppA
CalM	416	Regulatory protein		GTG/TGA	
CalN	398	Glycosyltransferase	3.4×10^{-79}	ATG/TGA	OleI
CalO	331	Hexopyranosyl-2,3-reductase	4.9×10^{-139}	ATG/TGA	EryBII
CalP	(179) ^d	Desaturase	5.7×10^{-7}	/TGA	CrtI
CalQ	453	UDP-D-glucose 6-dehydrogenase	confirmed ^c	GTG/TGA	
CalR	282	Transcriptional regulator	6.7×10^{-11}	ATG/TGA	SC5C7.03
CalS	1113	P ₄₅₀ oxidase	2.9×10^{-66}	GTG/TGA	Biol
CalT	432	oxygenase/halogenase	2.0×10^{-62}	GTG/TAA	PCZA361.2 ¹
CalU	377	glycosyltransferase	2.0×10^{-53}	ATG/TGA	SnogE/D
CalV	125	β-keto-acyl synthase III	2.0×10^{-65}	ATG/TGA	SC4A9
CalW	(449) ^d	cytochrome P450	1.0×10^{-91}	GTG/TGA	CYP105B1
CalX	(197) ^d	TDP-4-keto-6-deoxy-L-hexose 2,3-dehydratase	1.0×10^{-22}	/TGA	MtmV
6MSAS	(198) ^d	orsellinic acid synthase	6.5×10^{-76}	ATG/	
ActI	(207) ^d	polyketide cyclase	3.0×10^{-66}	/TGA	CurF
ActII	136	polyketide cyclase	5.0×10^{-53}	ATG/TGA	SchB
ActIII	(308) ^d	polyketide synthase	8.6×10^{-148}	GTG/	Pms1
orf1	322	unknown		ATG/TGA	
orf2	654	unknown		ATG/TGA	
orf3	373	integrase		3.0×10^{-13}	ATG/TGA
orf4	521	chromosome partitioning protein		3.3×10^{-10}	GTG/TAA
orf5	175	unknown		ATG/TGA	
orf6	139	unknown		ATG/TGA	
orf7	187	unknown		GTG/TGA	
orf8	266	regulatory protein		3.0×10^{-66}	ATG/TGA
OrfI	127	hydroxylase		1.5×10^{-7}	ATG/TGA
OrfII	248	unknown		GTG/TGA	SC4C6.24c
OrfIII	298	hydroxylase		3.3×10^{-90}	GTG/TGA
OrfIV	363	unknown		5.3×10^{-43}	GTG/TGA
OrfV	288	aminotransferase		2.9×10^{-37}	GTG/TGA
OrfVI	1012	glu-ammonia-ligase adenylyltransferase		exact	SCA32
OrfVII	236	Methyltransferase		8.0×10^{-63}	GTG/TAG
OrfVIII	441	Integral membrane protein		8.9×10^{-9}	GTG/TGA
OrfIX	478	Integral membrane protein		1.1×10^{-21}	ATG/TGA
OrfX	504	Membrane protein		5.5×10^{-20}	GTG/TGA
OrfXI	251	Immunity resistance protein		1.1×10^{-9}	B1496.F1.14
IS-element	1209 bp	insertional element		5.7×10^{-168}	TFXG IS1136 ¹¹¹

Fig. 3.

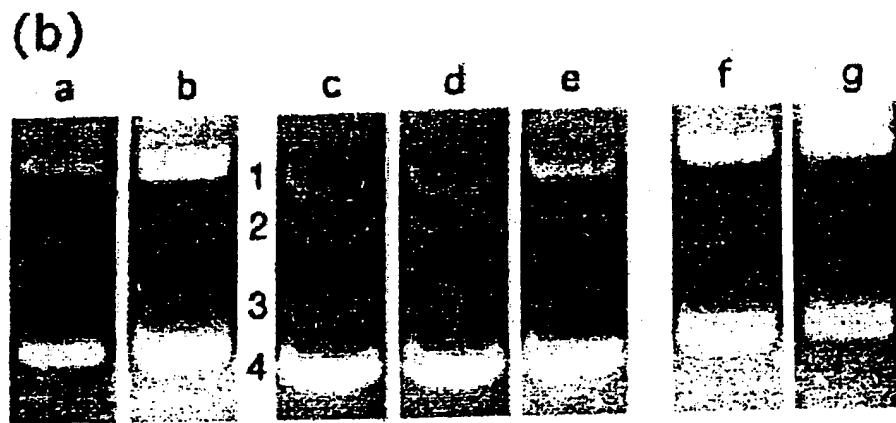
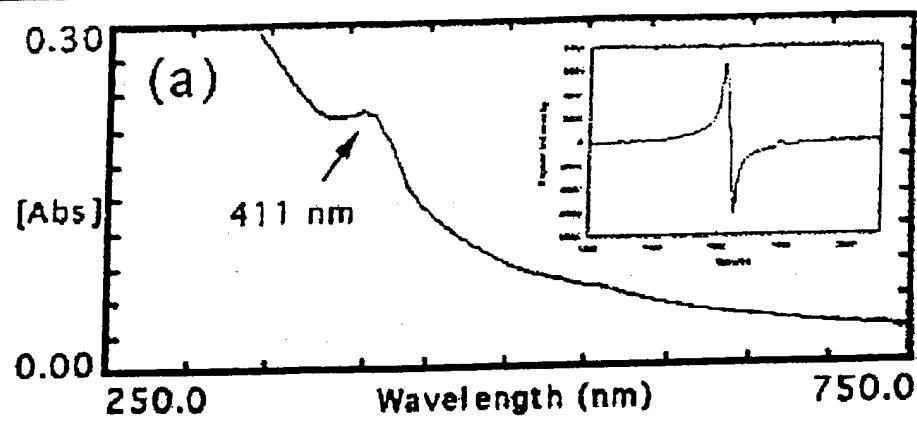


Fig. 4

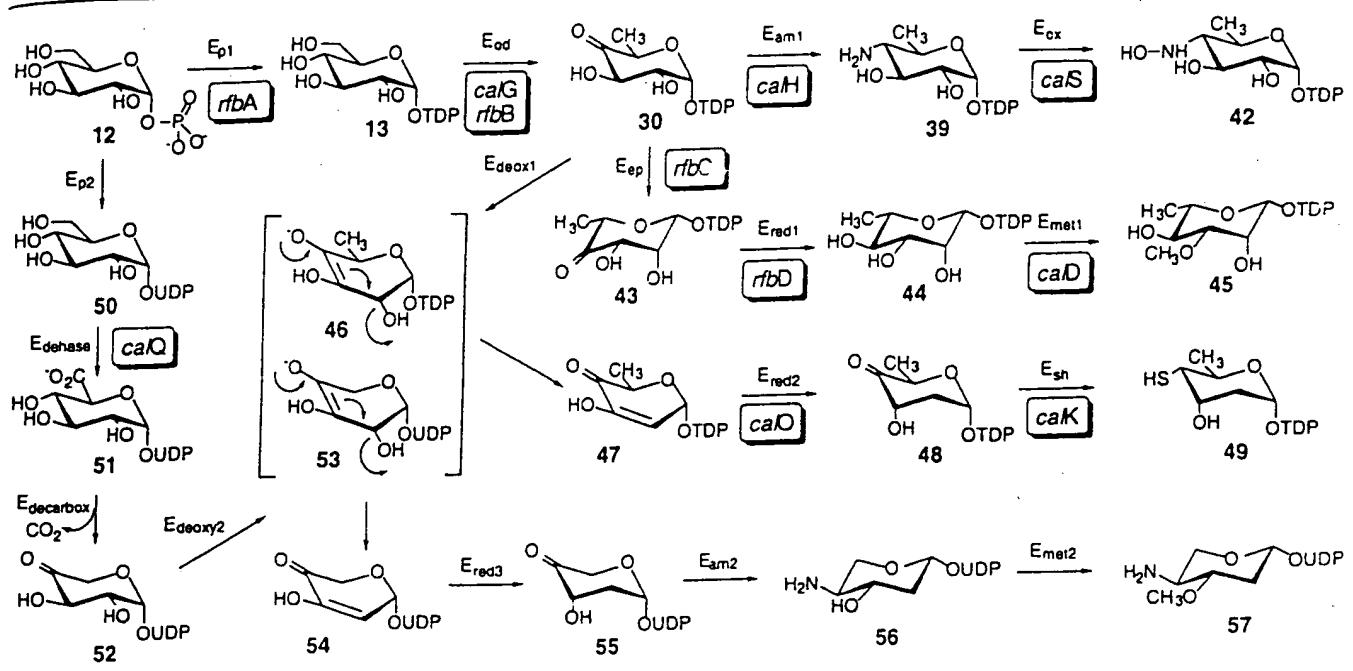


Fig. 5

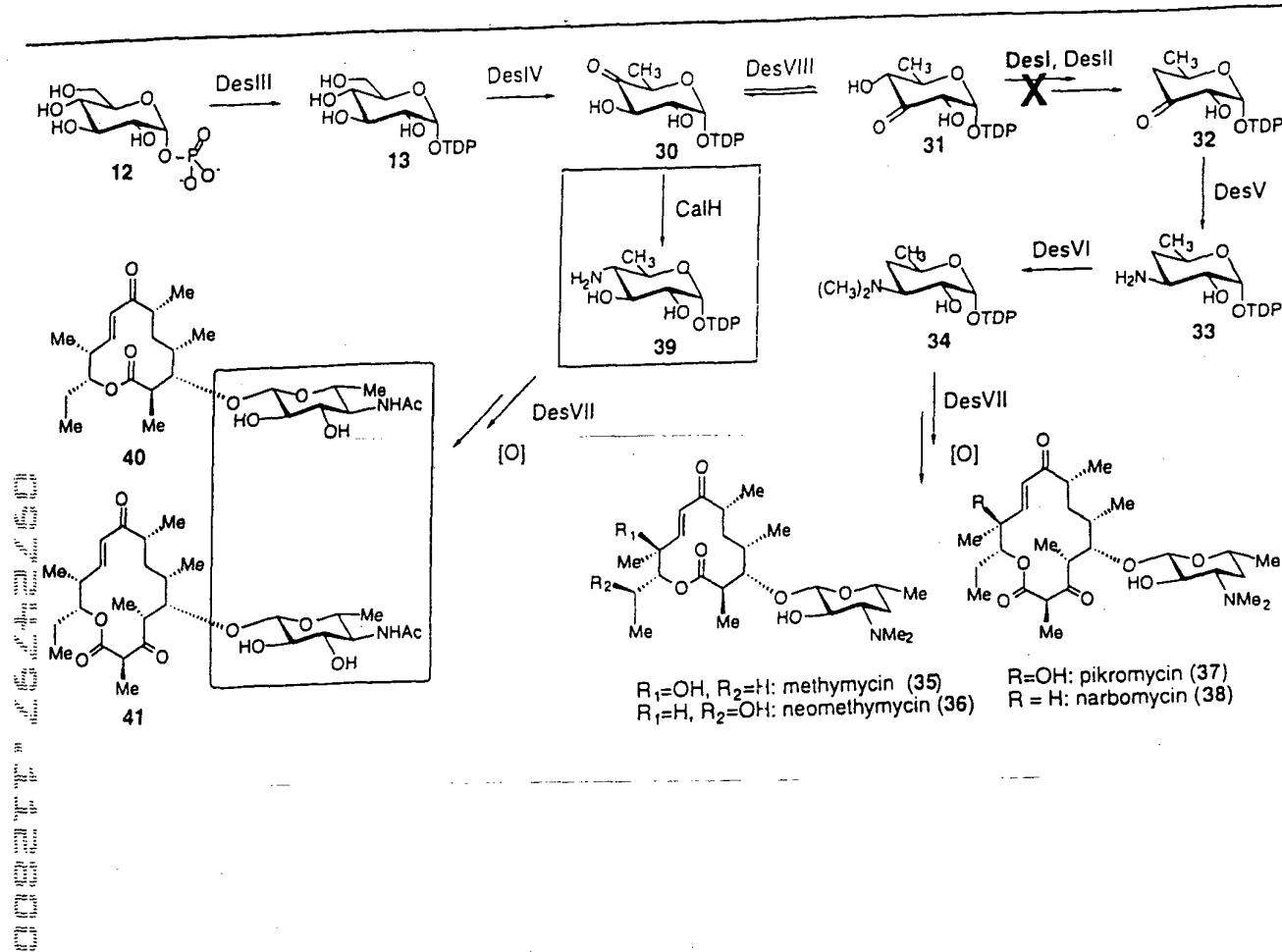


Fig. 6

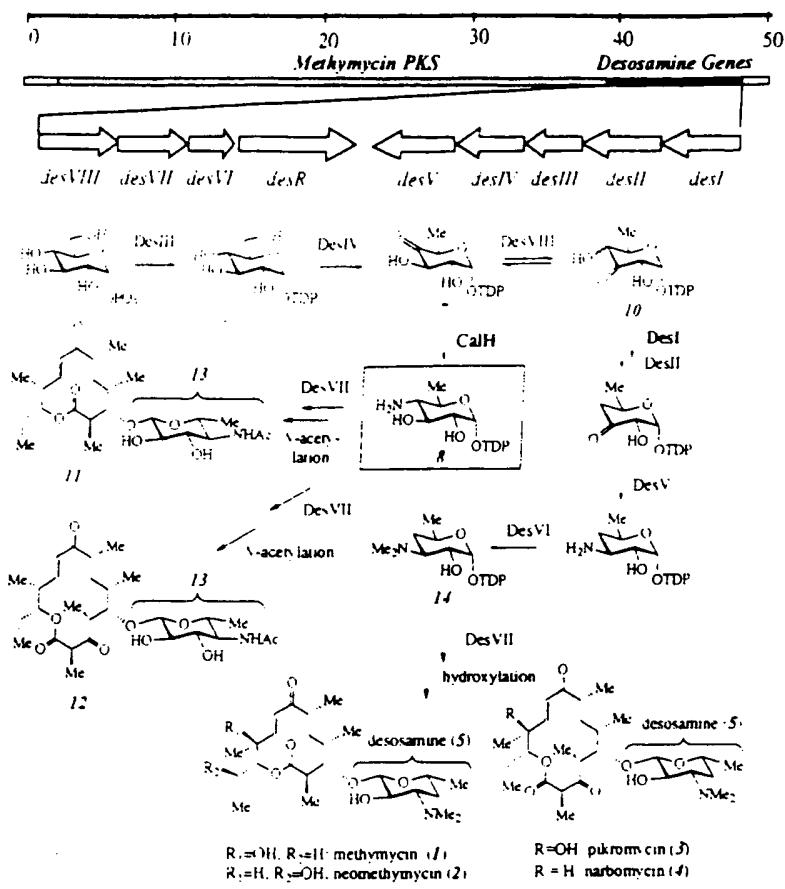


Fig. 7

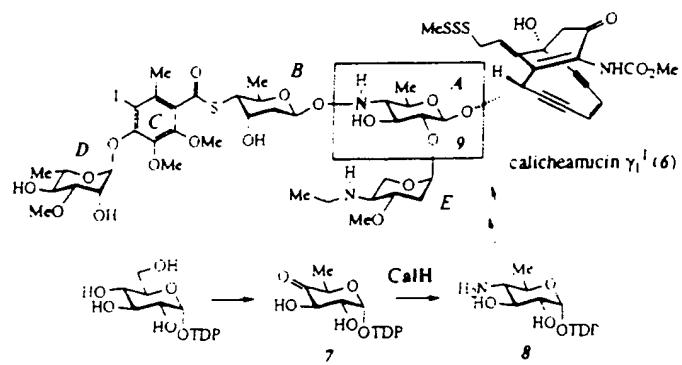


Fig. 8

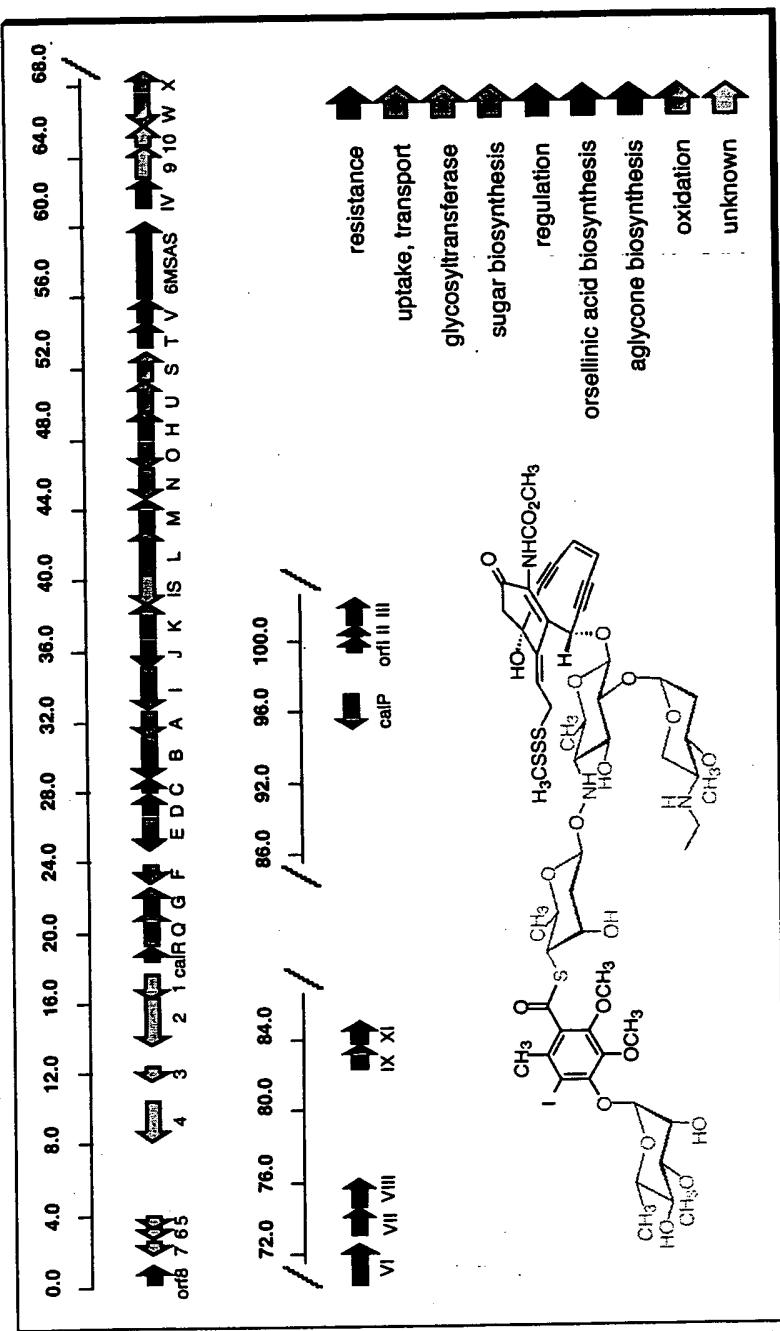


Fig 9

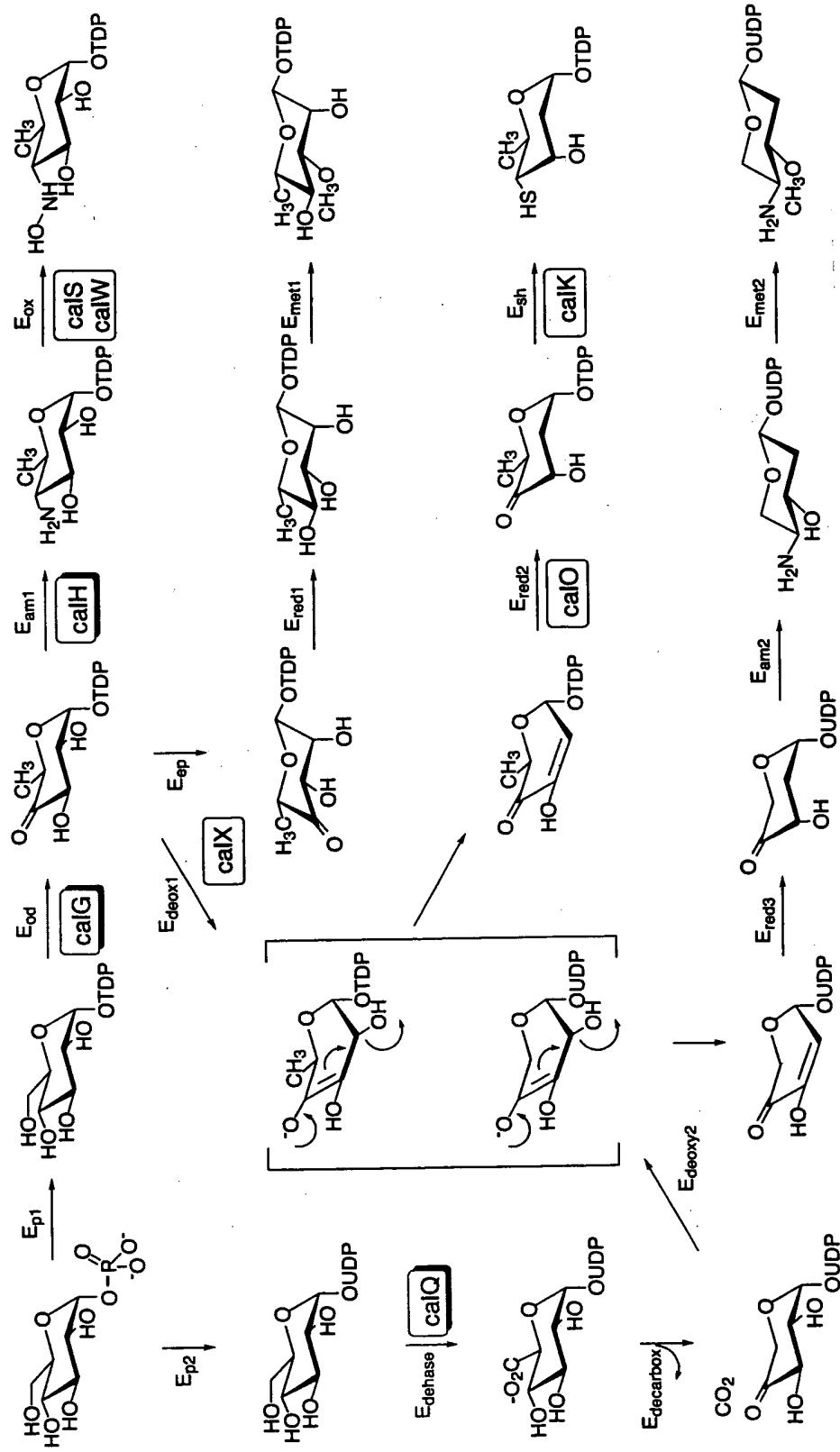
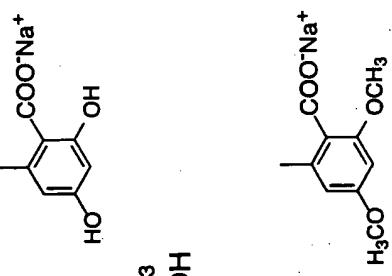
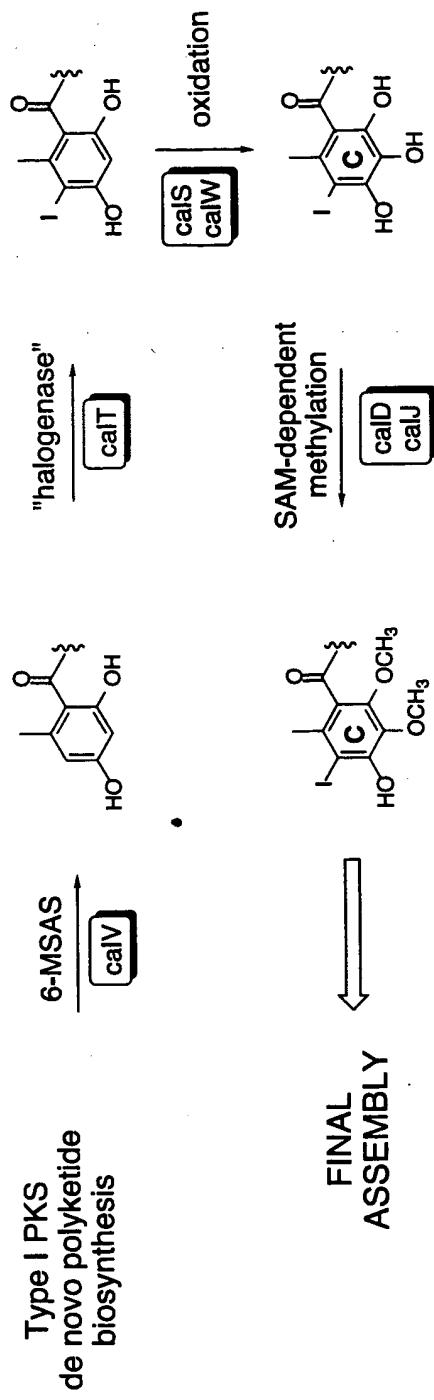


Fig. 10

The Aryltetrasaccharide Unit (a type I PKS product):



Synthesis of Putative Substrates:

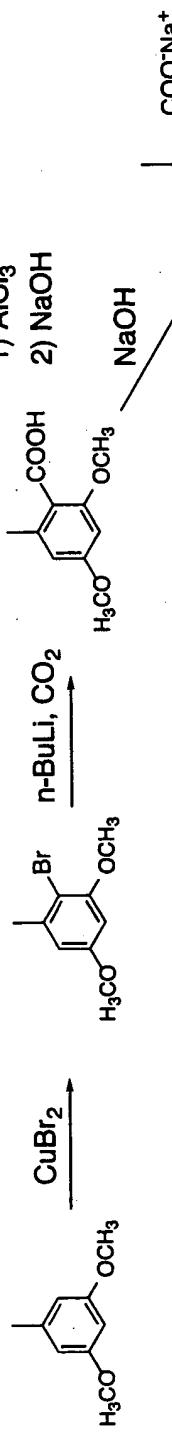


Fig 11

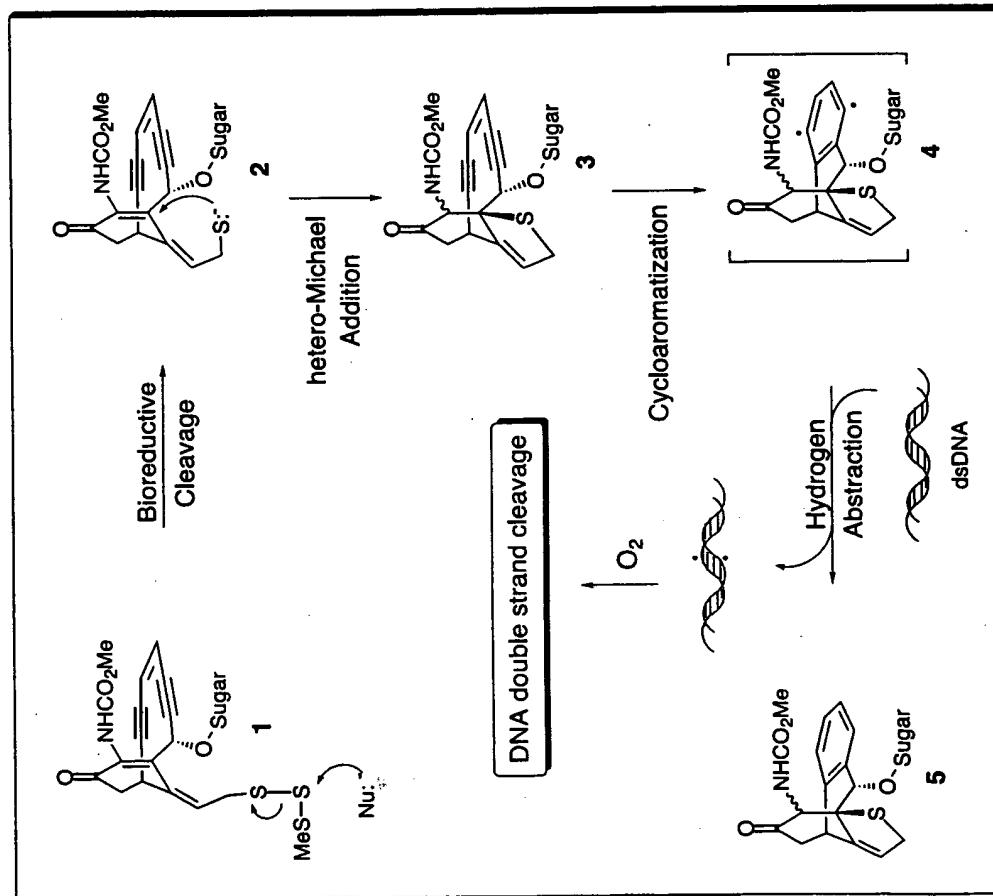
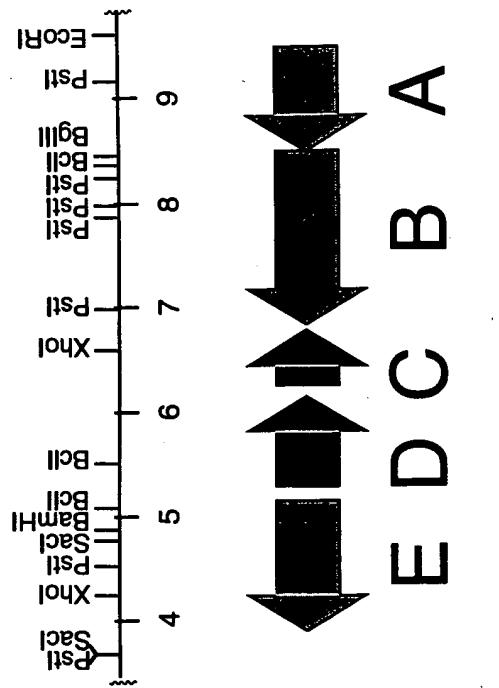


Fig 12

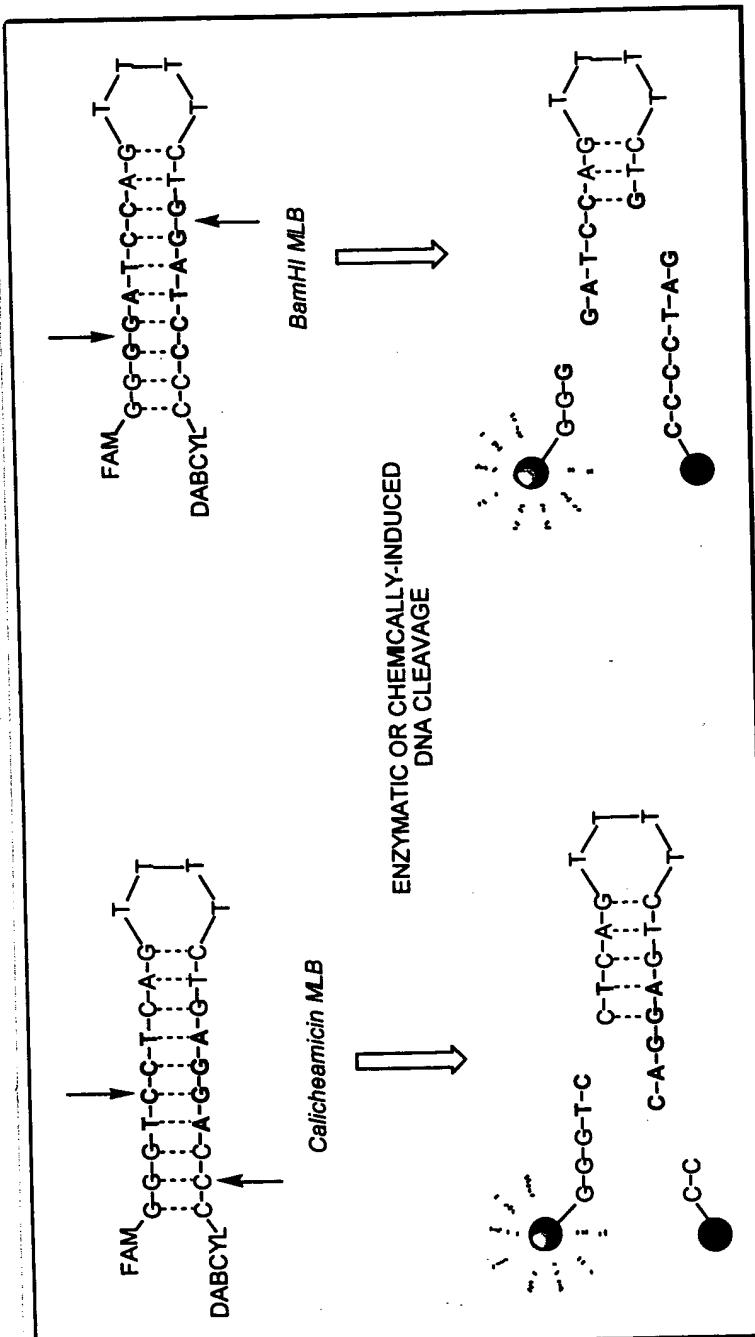


Fig 13

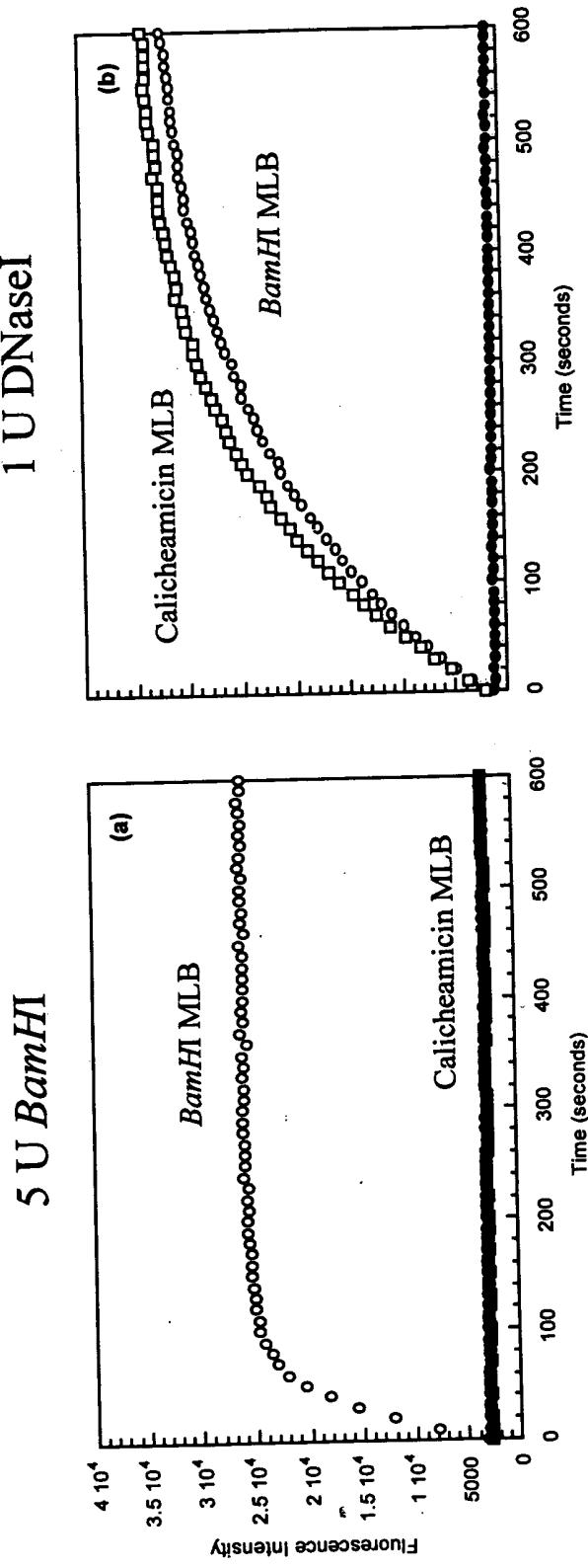


Fig 14

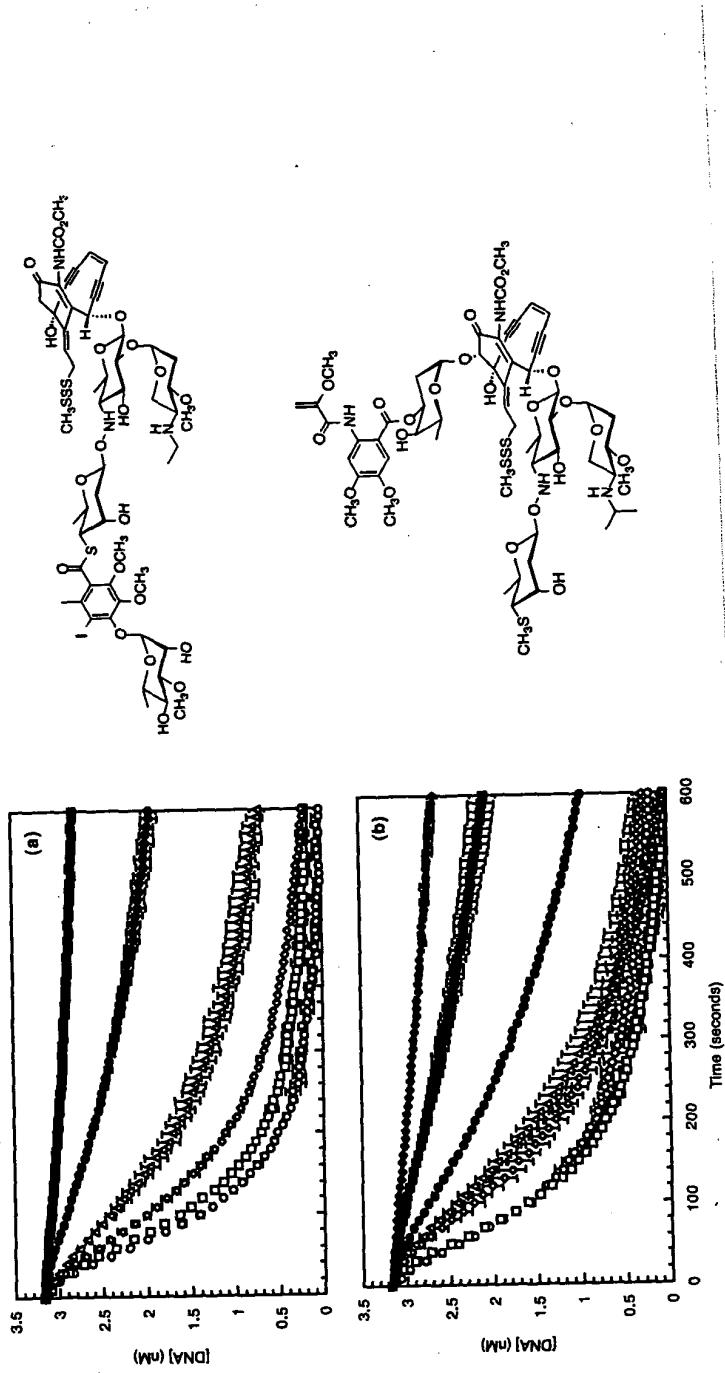


Fig 15

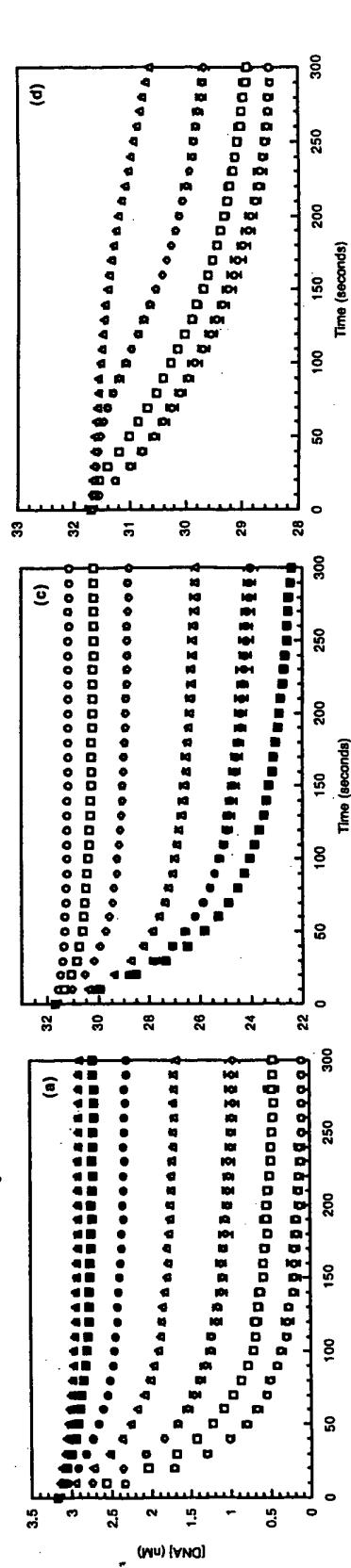
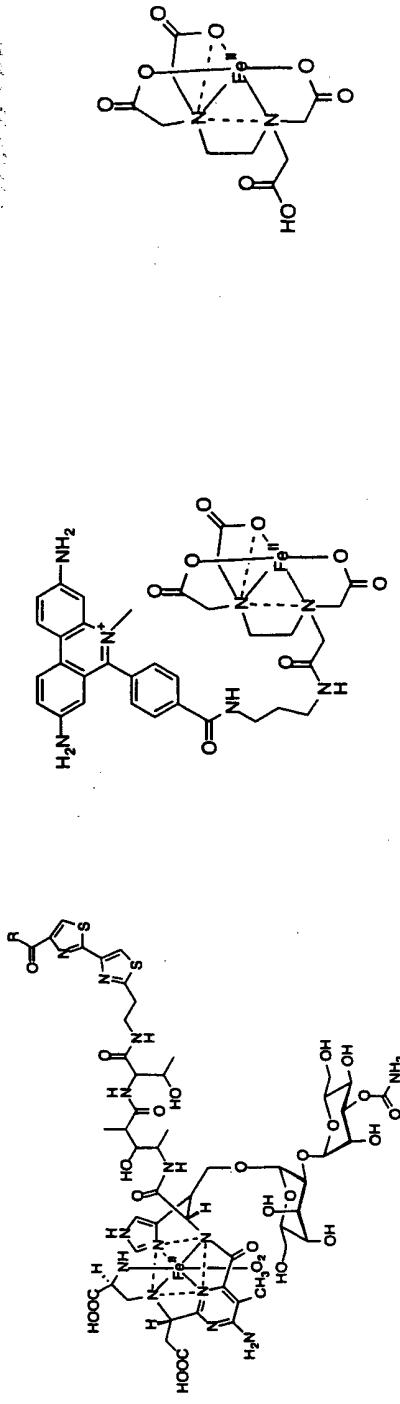


Fig 16

0.0 1.3 2.6 3.9 5.2

CaIC (nmol)

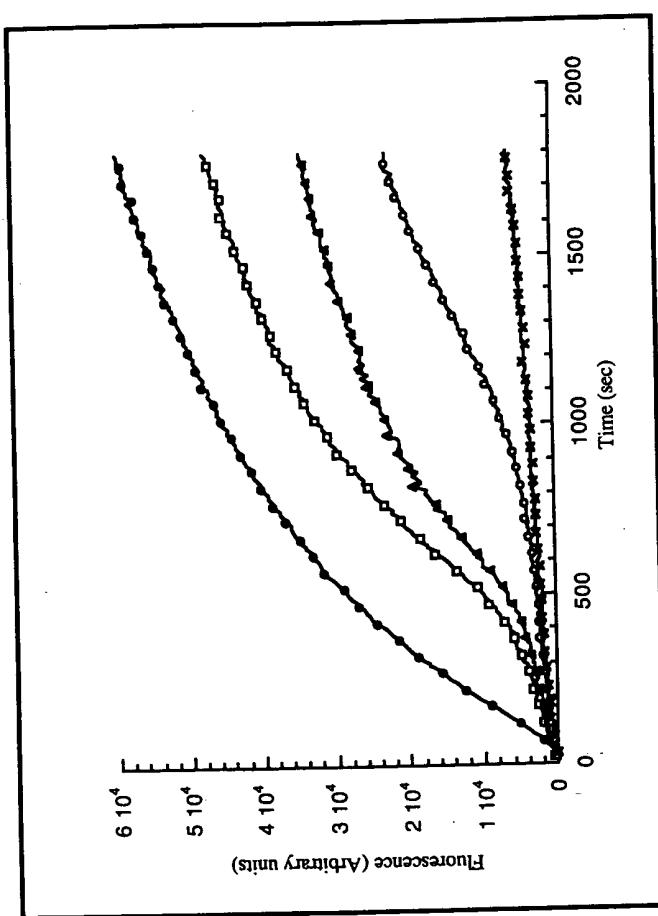


Fig 17

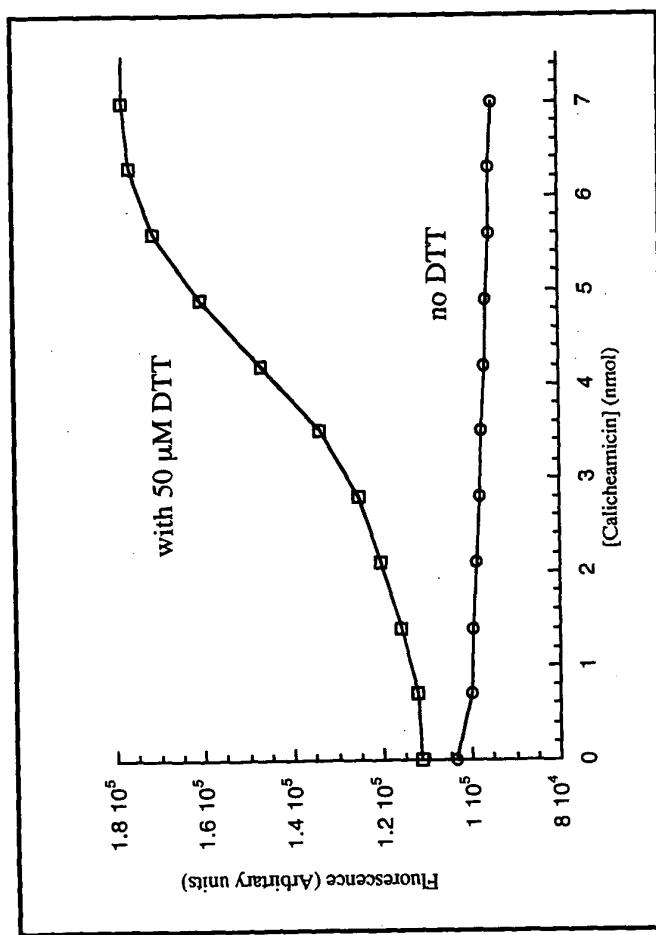
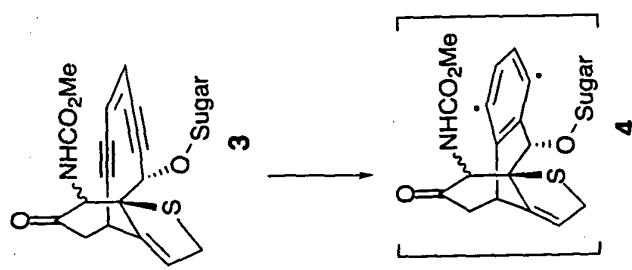


Fig 18